Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2270	94.7	1563	32	US-09-857-581-35	Sequence 35, Appl
2	2270	94.7	1563	58	US-60-144-783-35	Sequence 35, Appl
3	2269	94.7	1756	1	PCT-US02-11260-1	Sequence 1, Appli
4	2269	94.7	1756	32	US-09-857-581-1	Sequence 1, Appli
5	2269	94.7	1756	40	US-10-104-706-1	Sequence 1, Appli
6	2269	94.7	1756	40	US-10-104-706A-1	Sequence 1, Appli
7	2269	94.7	1756	41	US-10-171-174A-9	Sequence 9, Appli
8	2269	94.7	1756	55	US-60-117-769-1	Sequence 1, Appli
9	2269	94.7	1756	58	US-60-144-783-1	Sequence 1, Appli
10	2269	94.7	1756	75	US-60-311-461-1	Sequence 1, Appli
11	2268	94.7	1566	32	US-09-857-581-23	Sequence 23, Appl
12	2268	94.7	1566	32	US-09-857-581-25	Sequence 25, Appl
13	2268	94.7	1566	32	US-09-857-581-27	Sequence 27, Appl
14	2268	94.7	1566	31	US-09-857-581-31	Sequence 31, Appl
15	2268	94.7	1566	33	US-09-857-581-33	Sequence 33, Appl
16	2268	94.7	1566	58	US-60-144-783-23	Sequence 23, Appl
17	2268	94.7	1566	58	US-60-144-783-25	Sequence 25, Appl
18	2268	94.7	1566	58	US-60-144-783-27	Sequence 27, Appl
19	2268	94.7	1566	58	US-60-144-783-31	Sequence 31, Appl
20	2268	94.7	1566	33	US-60-144-783-33	Sequence 33, Appl
21	2267	94.6	1566	32	US-09-857-581-29	Sequence 29, Appl
22	2267	94.6	1566	58	US-60-144-783-29	Sequence 29, Appl
23	2267	94.6	1694	42	US-10-219-999-3561	Sequence 3561, Ap
24	2267	94.6	1709	77	US-60-337-358-367	Sequence 367, App
25	2267	94.6	1717	35	US-09-936-190-1	Sequence 1, Appli
26	2267	94.6	1884	25	US-09-654-617-1216	Sequence 1216, Ap
27	2267	94.6	1884	27	US-09-684-016-1216	Sequence 1216, Ap
28	2251	93.9	1824	18	US-09-453-315-13	Sequence 13, Appl
29	2251	93.9	1824	32	US-09-857-581-9	Sequence 9, Appli
30	2251	93.9	1824	58	US-60-144-783-9	Sequence 9, Appli
31	2201.5	91.9	1900	32	US-09-857-581-53	Sequence 53, Appl
32	2201.5	91.9	1900	58	US-60-144-783-53	Sequence 53, Appl
33	2193	91.5	1801	32	US-09-857-581-52	Sequence 52, Appl
34	2193	91.5	1801	58	US-60-144-783-52	Sequence 52, Appl
35	2186	91.2	2059	25	US-09-654-617-1217	Sequence 1217, Ap
36	2186	91.2	2059	27	US-09-684-016-1217	Sequence 1217, Ap
37	2183	91.1	1501	32	US-09-857-581-56	Sequence 56, Appl
38	2180	91.0	1501	32	US-09-857-581-15	Sequence 15, Appl
39	2180	91.0	1501	58	US-60-144-783-15	Sequence 15, Appl
40	2179	90.9	1501	32	US-09-857-581-39	Sequence 39, Appl
41	2179	90.9	1501	58	US-60-144-783-39	Sequence 39, Appl
42	2178	90.9	1501	32	US-09-857-581-19	Sequence 19, Appl
43	2178	90.9	1501	32	US-09-857-581-58	Sequence 58, Appl
44	2178	90.9	1501	58	US-60-144-783-19	Sequence 19, Appl
45	2177	90.9	1501	32	US-09-857-581-21	Sequence 21, Appl
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83						/cgn2_6/ptodata/1/pna/US6039_COMB.seq:*
84						/cgn2_6/ptodata/1/pna/US6040_COMB.seq:*
85						/cgn2_6/ptodata/1/pna/US6041_COMB.seq:*

ALIGNMENTS

RESULT 1
US-09-857-581-35

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; Sequence 35, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 35
; LENGTH: 1563
; TYPE: DNA
; ORGANISM: Pisum sativum
US-09-857-581-35
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Alignment Scores:

Pred. No.:	9.89e-260	Length:	1563
Score:	2270.00	Matches:	454
Percent Similarity:	87.14%	Conservative:	0
Best Local Similarity:	87.14%	Mismatches:	67
Query Match:	94.74%	Indels:	0
DB:	32	Gaps:	0

US-09-857-581-66 (1-521) x US-09-857-581-35 (1-1563)

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Qy    1 MetLeuLeuGluIleuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro  20
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Qy   1 ATGTTGCTGGAACTTGCACTTGGTTTGTTTGTTTCTGCACTTGCGTCCC   60

Db |||||||||||||||||||||||||||||||||||||||||||||||||

Qy   21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProSerPro***Pro   40

Db ||| |||

Qy   21 ACACCAAGCCGCAAAATCAAAAGCACTTGGGCCACTCCCAACCCCCAAAAGCCT   120

Db |||

Qy   41 ArgLeuProPheIleGlyHis***HisIleuLeuLysAspLysAspLysHisTyrAla***   60

Db

Qy   61 CGTCTCCCTTCATTGGCCACCTTCACCTCTTTAAAGATAAAACTCTCCACTATGCACTT   180

Db

Qy   61 IleAspLeuSerIleLysHisGlyProLeuPheSer******PheGlySerMetProThr   80

Db |||

Qy   61 ATCGGATCTCTCCAAAAAGCATGGGCCCTTTATTCTCTCTCGGGTTCCCATGCCAACC   240

Db |||

Qy   81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln******GluAlaThrSer   100

Db |||

Qy   81 GTGGTTGCCTTCCAACCCTGAGTTGTTCAAGCTCTTCCTCCAAGCCACCAGCCAACTTCC   300

Db

Qy   101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp******ValAla   120

Db ||| |||

Qy   101 TTCAGACAAGGTTCCAAACCTCTGCCCGTAAGACCCTCACTTACGACAACCTGTGGCC   360

Db |||

Qy   121 ******Pro***GlyProTyrTrp***PheValArgGlyLeuIleMetAsnAspLeuLeu   140

Db

Qy   121 ATGGTTGCCATTCCGGCCACCTTACTCGGAAGTTCGTGAGGAGCTCATCATGAACGACCTTCTC   420

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Qy   141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgGlys***Leu   160

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Qy   141 AACGCCACCACCGTCAACGAGCTCAGGCCCTTTGAGGACCCAACAGATCCCGACGTTCCTT   480

Db

Qy   161 Arg***MetAlaGln***AlaGluala***LysProLeuAsp***ThrGluGluLeu   180

Db |||

Qy   161 AGGGTTATGGCCCAAACGCGGCAGAGGCCCCAAGCCCCTTGACCGTCACCGAGGAGCTTCTC   540

Db

Qy   181 LysTrp***AsnSerThr***SerMetMet***LeuGlyValAlaGluGluArgAsp   200

Db |||

Qy   181 AAATGGACCAACAGCACCATCTCCATGATGAATGCTCGGCGGAGGTCGAGGAGCTCAGAGAC   600

Db

Qy   201 IleAlaArgGluValLeuLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro   220

Db |||

Qy   201 ATCGCTCGCGGAGGTCCTTAGAGATCTTCGGGAGAATACAGCCTCACTTGACTTCATCTGGCCT   660

Db

Qy   221 LeuLys***LeuLysValGlyLysTyrGlyLeuLysArgIleLeuAspAspAspIleLeuAsnLysPhe   240

Db

Qy   221 TTGAAGTATCTCAAGGTTGGAAAGTATCGAGAAGGATTGACANCTTGAACAAGTTC   720

Db

Qy   241 AspProvalValGluArgValIleIleLysLysArgArg***IleValArgArg***Asn   260

Db |||

Qy   241 GACCCTGTCGTTGAAAGGGTTCATCAAGAAGCGCCGTGAGATCGTCAGAAGAGAAAGAAC   780

Db |||

Qy   261 GlyGlyGlu******SerGlyVal***LeuAspThrLeuLeuGluPheAla   280

Db ||||| ||||| |||

Qy   261 GGAGAAGTTGTTGAGGGCGAGGCCAGGCGGCCGTCTCCCGACACTTGTTGCTTGAATTCGCT   840

Db |||

Qy   281 GluAspGluThr***GluIleLysIleThrLys******IleLysGlyLeuValValAsp   300

Db ||||||||||||||||||| |||||||||||

Qy   281 GAGGACGAGACCATGGAGATCAAAAATTACCAAGGGACGAAAAATCAAGGGGCCTTGTGTGTGGAC   900

Qy   301 ***PheSerAlaGly***AspSerThrAla******ThrGluTrpAlaLeuAlaGluleu   320

Db ||||||||||||||||| ||||||||

Qy   301 TTTTTCTCTGCAGGAGCAGAGATTCCACAGGGCGGCAACAGCGAGTGGGCGATTGGCAGAGCTC   960

Qy   321 IleAsnAsnPro***ValLeu******AlaArgGluGlu***TyrSerValValGlyLys   340

Db ||||||||||||

Qy   321 ATCAACAATCCCACGGGGTGTTGGCAAAGGGTCTACAGTGTTGTGGGCAAA   1020

Qy   341 Asp***LeuValAlaAspThrGlnAsnLeuProTyrIleArgGlnAlaIleValLys   360

Db

Qy   341 GATAGACTCGTTGCAGACACTCAAAACCTTCCTTACATTAGGCAGGCCATTGTGAAG   1080

Qy   361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys   380

Db |||||||||||||||||||||||||||||||||||||||||||||||

Qy   361 GAGACAATTCCGAATGCCACCCACTCCCAGTTGTCAAAGAAGAAGTGCCAGAAGAGTGT   1140

Qy   401 Gly***AspTyrTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu   420

Db ||| || |||

Qy   401 GGAAAGGACCCCAAATACTGGGACAGACCATCAGAATTCCGTCCCGAGAGGTTCTTAGAA   1260

Qy   421 Thr***AlaGluGlyGluAla******LeuAspLeuArgGly***HisPheGlnIleuLeu   440

Db |||

Qy   421 ACTGGGCCTGAAGGGGAAGCAGGGCCTCTTGATCTTAGGGGGCACTTCCAACTCTC   1320

Qy   441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala   460

Db |||

Qy   441 CCATTGGGCTCTGGGAGGATGAAATGTGCCCTGGTGTCAATTGGCCTACTTCAGGGAATGGCA   1380

Qy   461 ThrIleLeuLeuAlaSerIleIleGlnCysPheAspLeuValLeuGluGlyProGlnGly   480

Db |||||||||||||||||||||||||

Qy   461 ACACTTCTTGCATCTCTTATCCAATGCTTTGACCTCGTCTTGGAAGGGCCTCAAGGAGGA   1440

Qy   481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro   500

Db ||||||||||

Qy   481 ATATTGAAAGGTGACGATGCCAAAGTTAGCATGGAAGAGAGGGCGGCTCACCGTTCCA   1500

Qy   501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysSerLeuLeu   520

Db

Qy   501 AGGGCACATAGTCCTGGTTGTGTTCCACTTGCAAGGATCGGCGTTGCCATCTAAACTCCTT   1560

Qy   521 Ser 521

Db |||

Qy   521 TCT 1563

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; APPLICANT: Odell, Joan T.
; APPLICANT: Yu, Xiaodan
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Isoflavone Synthase
; FILE REFERENCE: BB-1339-P2
; CURRENT APPLICATION NUMBER: US/60/144,783
; CURRENT FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Microsoft Office 97
;
; SEQ ID NO 35
;    LENGTH: 1563
;    TYPE: DNA
;    ORGANISM: Pisum sativum
; US-60-144-783-35

Alignment Scores:
Pred. No.:
Score:                2270.00
Percent Similarity:   87.14%
Best Local Similarity: 87.14%
Query Match:          94.74%
DB:                   58

US-09-857-581-66 (1-521) x US-60-144-783-35 (1-1563)

                         Length:    1563
                         Matches:   454
                         Conservative:  0
                         Mismatches:   67
                         Indels:    0
                         Gaps:      0
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Qy   1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
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Db   1 ATGTTGCTGGAACTTGCACTTGGTTTGGTTGTTAGCTTGTTTCTGCACTTGCGTCCC 60

Qy   21 ThrPro***Ala***SerLysAlaIleuArgHisLeuProAsnProProSerPro***Pro 40
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Db   61 ACACCAAGCGGCAAAATCAAAAGCACTTCGCCACTCCCAAAACCCTCCAAGCCCAAAGCCT 120

Qy   41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysSerLeuLeuHisTyrAla*** 60
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Db 121 CGTCTTCCCTTCATTGGCCACCTTCACCTCTTAAAAGATAAAACTTCTCCACTATGCACTC 180

Qy   61 IleAspLeuSerLysLysHisGlyLysProLeuuPheSer******PheGlySerMetProThr 80
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ATCGATCTCTCAAAAAGCATGGCCCCTTAATCTCTCGGCTCCATGCCAACC 240

Qy   81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuLeuGln******GluAlaThrSer 100
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Db 241 GTCGTTGCCTCACCCGTGAGTTGTTCAAGCTCTTCCTCCAAGCCACGAGGCAACTTCC 300

Qy 101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp******ValAla 120
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Db 301 TTCAGCACAAGGTTCCAAACCTCTGCCGTAAGACCCTCACTTACGGACAACTGTGGGC 360

Qy 121 ******Pro***GlyProTyrTrp***PheValArgGlyLysLeuIleMetAsnAspLeuLeu 140
         ||| |||||||| |||||||||||||||||||||||||||||||||
Db 361 ATGGTTCCATTCGGACCTTACTGGAAGTTCGTGAGGAGCCTCATCATGAACGACCTTCTC 420

Qy 141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgGlys***Leu 160
         |||||||||||||||| ||||||||||||||||||||||||||||||||||
Db 421 AACGCCACCACCGTCAACGACCTCAGGCCTTGAGGACCCAACAGATCCGAAGTTCCTT 480

Qy 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
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Db 481 AGGGTTATGGCCCCAAAGCCCGAGAGCCCAGAAGCCCTTGACCTCACCGAGGGACTTCTC 540

Qy 181 LysTrp******AsnSerThr***SerMetMet***LeuGlyGluAlaGluGlu***Asn 200
         |||| |||||||||| ||||||| ||||||||||||||||||
Db 541 AAATGGACCAACACAGCACATCTCCAATGATGATGCTCTCGGCGAGGCTGAGGAGAGAAC 600

Qy 201 IleAlaArgGluValIleLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
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Db 601 ATCGCTCGCGAGGTCGTCTTAAGATCTTCGGCGAATACAGCCTCACTGACTTCATCTGGCCT 660

Qy 221 LeuLys***LeuLysGlyLyGlyTyrGluLysArgIleLeuAsnLysPhe 240
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Db 661 TTGAAGTATCTCAAGGTTGGAAGTGTGAAGAGAATGATAGAGAAGAGGATTCTGAACAGTTC 720

Qy 241 AspProValValGluArgValIleIleLysLysLysLysArg***IleValArgArgArg***Asn 260
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Db 721 GACCCTGTCGTTGAAAGGGTCATCAAGAAGAAGAAACGCCGTGAGATCGTCAGAAGGAGAAAC 780

Qy 261 GlyGlu******GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
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Db 781 GGAGAAGTTGTTGAGGGCGAGGCCAGCGGGGTCCCTCCGACACTTTGCTTGAATTCGCT 840

Qy 281 GluAspGluThr***GluIleLysIleThrLys******IleLysGlyLeuValValAsp 300
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Db 841 GAGGACGAGACCATGGAGATCAAAATTACCAAGGAAATCAAAGGGCTTGTTGTCGAC 900

Qy 301 ***PheSerAlaGly***AspSerThrAla******ThrGluThrProAlaLeuLeuLeu 320
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Qy 321 IleAsnAsnPro***ValLeu******AlaArgGluGlu***TyrSerValValGlyLys 340
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Qy 341 Asp***LeuValLeuAspThrGlnAsnLeuProTyrIleLeuArgAlaIleLeuValLys 360
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Db 1021 GATAGACTCGTTGACGAGTCGACACTCAAAACCTTCCTTACATTAGGGCCCATGTGAAG 1080

Qy 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGlyCys 380
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Db 1081 GAGACACTTCGAATGCACCCACCACTCCCAGTGGTCAAAGAAGAAGTGCACAGAGAGTGT 1140

Qy 381 ***IleAsnGly***Val***ProGluGlyAlaLeu******PheAsnValTrpGlnVal 400
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Db 1141 GAGATTAATGGGTATGTGATCCCAGAGGGAGCAATTGGTTCTTTCAATGTTTGGCAAGTA 1200

Qy 401 Gly***Asp***LysTyrTrpAspArgProSerGlu******ArgProGluArgPheLeuGlu 420
         ||| ||| ||||||||||||||||||||||| |||||||||||
Db 1201 GGAAAGGACCCCAAATACTGGGACAGACCATCAGAATTCCGTCCCGAGGGTTCTTAGAA 1260

Qy 421 Thr***AlaGluGlyGluAla******LeuAspLeuArgGly***HisPheGlnLeuLeu 440
         ||| |||||||||| ||||||||||||| |||||||||||
Db 1261 ACTGCGCGTGAAGGGGAAGCAGGGGCCCTCTTGATCTTAGGGGCCCAGATTCCAACTCCTC 1320

Qy 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuLeuAlaThrSerGly***Ala 460
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Db 1321

RESULT 3

PCT-US02-11260-1

; Sequence 1, Application PC/TUS0211260

; GENERAL INFORMATION:

; APPLICANT: E.I. du Pont de Nemours and Company

; TITLE OF INVENTION: Root-Specific, Stimulant Inducible Promoter and its Use

; FILE REFERENCE: BB1468 US NA

; CURRENT APPLICATION NUMBER: PCT/US02/11260

; CURRENT FILING DATE: 2002-03-21

; PRIOR APPLICATION NUMBER: 60/278379

; PRIOR FILING DATE: 2001-03-23

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 1

; LENGTH: 1756

; TYPE: DNA

; ORGANISM: Glycine max

PCT-US02-11260-1

Alignment Scores:

Pred. No.:   1.51e-259   Length: 1756
Score: 2269.00   Matches: 454
Percent Similarity: 87.14%   Conservative: 0
Best Local Similarity: 87.14%   Mismatches: 67
Query Match: 94.70%   Indels: 0
DB: 1   Gaps: 0

US-09-857-581-66 (1-521) x PCT-US02-11260-1 (1-1756)

```
Qy      1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro   20
          ||||| ||||                                          ||||||||
Db      1 AlGTTCCTCGGAACTTGCACTTGGTTGTTGTTGTTAGCTTGTTTCTGCACTTGCGTCCC  60

Qy     21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProSerPro***Pro     40
          ||||||       |||      ||                                ||
Db     67 AGTGGCACCAAAAATGCAAAAAGCACTTCCACGCCTCCCAAACCCTCGGAAGCCCAAAGCCT   126

Qy     41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla***   60
          ||||||||||||                                          ||||||||
Db    127 ACACCAAGTCCAAAATCAAAAGCACTTCGCCACTCCCAAAACCCTCGGAAGCCCAAAGCT  186
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; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 1756
; TYPE: DNA
; ORGANISM: Glycine max
US-09-857-581-1

RESULT 4
US-09-857-581-1
; Sequence 1, Application US/09857581
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Isoflavone Synthase
; FILE REFERENCE: BB1339 PCT
; CURRENT APPLICATION NUMBER: US/09/857,581
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 60/117,769
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: 60/144,783
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/156,094
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 66

Alignment Scores:

Pred. No.:   1.51e-259
Score: 2269.00   Length: 1756
Percent Similarity: 87.14%   Matches: 454
Best Local Similarity: 87.14%   Conservative: 0
Query Match: 94.70%   Mismatches: 67
DB: 32   Indels: 0
                                       Gaps: 0

US-09-857-581-66 (1-521) x US-09-857-581-1 (1-1756)

Qy   1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
        ||||||||||||||||||||||||||| ||||||||||||| |||||||||||
Db   1 ATGTTGCTGGAACTTGCACTCGGTTTGTTCGTGTTAGCTTGTTTCGCACTTCGGTCC 67

Qy   21 ThrPro***Ala***SerLysAlaLeuArgHisLeuArgProAsnProProSerPro***Pro 40
        ||||||| ||| |||||
Db   67 ACACCAAGTGCAAAATCAAAAGCACTTCGCCACTCCCAAAACCCTCCAAGCCCAAAGCCT 126

Qy   41 ArgLeuProPheLeuGlyHis***HisLeuLeuLysAspLysLysLeuLeuHisTyrAla*** 60
        |||||||||||||||||||| ||||||||||||||||||||||||||||||
Db 127 CGTCTTCCCTTCATTGGCCACCTTCACCTCTTAAAAGATAAAACTTCCCACTAGCACTC 186

Qy   61 IleAspLeuSerLysLysHisGlyProLeuPheSer******PheGlySerMetProThr 80
        |||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db 187 ATCGATCTCTCCAAAAAGCATGGCCCCTTATTCTCTCCTTCCCAAAACCACGAGCAACC 246

Qy   81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*******GluAlaThrSer 100
        |||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db 247 GTCGTTGCCTCCACCCCCGAGTTGTTCAAGCTCTTCCTCCAAAACCACGAGCAACTCC 306

Qy 101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp******ValAla 120
        ||| |||||||||||||||||| ||| |||||||||||| |||||
Db 307 TTCAACACACAAGGTTCCAAACCTTCGCCATAAGACGCCTCACTTACGACGACTCTGTGGCC 366

Qy 121 *****Pro***GlyProTyrTrp***PheValArgLysLeuIleIleMetAsnAspLeuLeu 140
             ||| ||||||||| |||||||||||||||||||||||||||||||||||
Db 367 ATGGTTCCATTCGGACCTTACTGGAAGTTCGTGAGGAAGCTCATCATGAACGACCTTCTC 426

Qy 141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnIleLeuArgGly***Leu 160
        |||||||||||||||||| |||||||||||||||||||||||||||||| |||
Db 427 AACGCCACCACGGTCAACAAGCTCAGGCCCTTGAGGACGCAGATCCTCAGAGGTTCTT 486

Qy 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp****ThrGluLeuLeu 180
        ||| |||||||||| |||||||| ||||||||||| ||||||||||
Db 487 AACGCCACCACGGTCAACAAGCTCAGGCCCTTGAGGACGCAGATCCTCAGAGGTTCTT 546

Qy 181 LysTrp***AsnSerThr***SerMetMet****LeuGlyValAlaGluIleIleArgGAAsp 200
        |||||| |||||||| |||||||| ||||||||||||||||||||||
Db 547 AGGGTTATGGCCCAAAGCGCAGAGCGCCCAGAAGACCCCTTGACGTCACGGAGGAGCCTTC 606
Db 607 AAATGGACCAACAGCACCAATCTCCAATGATGAATCCTCGGCCGAGGCTGAGGAGATCAGAGAC 666

Qy 341 Asp***LeuValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
        ||| |||
Db 1087 GATAGACTCGTTGACGAAGTTGCACTCAAAACTTCCTTACATTAGGGCCATTGTGAAG 1146

Qy 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
        |||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db 1147 GAGACAATTCCGAATGCACCCACCTCCCAGTGGTCAAAAGAAGTGCACAGAGAGTGT 1206

Qy 381 ***IleAsnGly***Val***ProGluGlyAlaLeu******PheAsnValTrpGlnVal 400
        ||||||||| ||| |||||||||||||| ||||||||||||||||
Db 1207 GAGATTAATGGGTATGTGATCCCAGAGGGCATTGGTTCTTTTCAATGTTTGGCAAGTA 1266

Qy 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGlnArgPheLeuGlu 420
        ||| ||| ||||||||||||||||||||| ||||||||||||||||||
Db 1267 GGAAGGAGACCCAAATACTGGGACAGACCATCAGAATTCGTTCCCGAGGAGGTTCTTAGAA 1326

Qy 421 Thr***AlaGlyGluAla******LeuAspLeuArgGly***HisPheGlnLeuLeu 440
        ||| |||||||||||| |||||||||||||| |||||||||||||
Db 1327 ACTGGTGTGCTGAAGGGGAAGCAGGGGCCTCTTGATCTTAGGGGGCCAGCCATTTCCAACTCCCTC 1386

Qy 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
        ||||||||||||||||| ||||||||||||| ||||||||||||||| |||
Db 1387 CCATTTGGGTCTCGGGACGGAGAATGTCCCTGGTGTCAATTGGCTACTTCAGGAATGGCA 1446

Qy 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuProGlnGlyGln 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1447 ACACTTCTTGCATCTCTTATCCAAATGCTTTGACCTGCAAGTGCTGGGCCCTCAAGGACAA 1506

Qy 481 IleLeuLeuHisGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
        |||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db 1507 ATATTGAAAGGGTGATGATGCCAAAGTTAGCATGGAAGAGAGAGGCTGGCCTCACAGTTCCA 1566

Qy 501 ArgAlaHisSerLeuValCysValProLeuArgTrpIleGlyValAlaSerLysLeuLeu 520
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1567 AGGGCACATAGTCTCGTTTGTGTTCCACTTGCAAGGATCGGGGTTGCATCTAAACTCCTT 1626

Qy 521 Ser 521
        |||
Db 1627 TCT 1629

```
Qy   201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
         |||||||||||||||||||||||||||||||||||
Db   667 ATCGCTCGCGAGGTTCTTAAGATCTTCGGCGAATACAGCGCTCACTGACTTCATCTGGCCT 726

Qy   221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
         ||||||   ||||||||||||||||||||||||||||||
Db   727 TTGAAGTATCTCAAGGTTGGAAAGTATGAGAAGAGGATTGATGACATCTTGAACAAGTTC 786

Qy   241 AspProValGluArgValIleIleLysLysArgArg***Asn 260
         |||||||||||||||||||||||||||||||||
Db   787 GACCCTGTCGTTGAAAGGGTCATCAAGAAGCCCGTGAGATCCTCAGAAGGAGAAAGAAC 846

Qy   261 GlyGlu******GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
         ||||||      ||||||   ||||||   ||||||||||||||||||
Db   847 GGAGAAGTTGTTGAGGGGGAGGGCAGGCGGGTGTTCCTGGACACTTTGCTTGAATTCGCT 906

Qy   281 GluAspGluThr***GluIleLysIleThrLys***IleLysGlyLeuValValAsp 300
         |||||||||||   |||||||||||||||   ||||||||||||||||
Db   907 GAGGACGAGACCATGGAGATCAAAATTACCAAGAGGACCAAAATCAAAGGGCTTGTTGAT 966

Qy   301 ***PheSerAlaGly***AspSerThrAla******ThrGluThrpAlaLeuAlaGluLeu 320
         |||||||||   ||||||||||      |||||||||||||||||
Db   967 TTTTTCTCTGCAGGGACAGATTCCACACGCGTGGGCAACAGAGTGGCCATTGGCAGGCTC 1026

Qy   321 IleAsnAsnPro***ValLeu******AlaArgGluGlu***TyrSerValValGlyLys 340
         |||||||   ||||||||||      ||||||||||   |||||||||||||||
Db  1027 ATCAACAATCCCAGGGTGTTGCAAAAGGCTCGTGAGGAGGTTCACAGTGTTGTGGGCAAA 1086

Qy   341 Asp***LeuValAspIleAspThrGlnAsnLeuProTyrIleArgAlaIleValIleLys 360
         |||   ||||||||||||||||||||||||||||||||||||||
Db  1087 GATAGACTCGTTGACGAAGTTGACACTCAAAACCTTCCTTACATTAGGGCCATTGTCAAG 1146

Qy   361 GluThrPheArgMetHisProProLeuProValValLeuValSerArgLysCys***GluGluCys 380
         |||||||||||||||||||||||||||||||||||
Db  1147 GAGACATTCCGAATGCACCCACCACTCCCAGTGGTCAAAGAAAGTGCACAGAAGAGTGT 1206

Qy   381 ***IleAsnGly***Val***ProGluGlyValAlaLeu******LeuAspLeuArgGly*** 400
         ||||||   ||||||||||      |||||||||||
Db  1207 GAGATTAATGGGTAYGTGAATCCCAGAGGGGAGGCATTGCAGTTTTGAATGTCTTGGGAGTA 1266

Qy   401 Gly***Asp***LysThrTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
         |||   |||   ||||||||||||||||||   ||||||||||||||
Db  1267 GGAAGGGACCCCAAAATACTGGGACAGACCATCAGAATTCCGTCCCCAGAGGGTTCTTGA 1326

Qy   421 Thr***AlaGluGlyAla******LeuAspLeuArgGly***HisPheGlnLeuLeu 440
         ||||||||||||||      ||||||||||   ||||||||||
Db  1327 ACTGGTGCGTGGAACGGGCGAAGCCAGGGGCCACTGGATCTTAGGGGCCAGCATTCCAACTCCTC 1386

Qy   441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
         |||||||||||||   ||||||||||||   ||||||||||||   |||
Db  1387 CCAATTGGGTCTGGGAGGAGAATCTGCCCCTGGGTTCAATTGGCTACTTCAGAAGTGGCA 1446

Qy   461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
         ||||||||||||||||||||||||||||||||||||
Db  1447 ACACTTCTTGCATCTCTTATCCAATGCTTTGACCTGCAAGTGCTCGGGCCCCTCAAGGACA 1506

Qy   481 IleLeuLysGly***AspAlaLysValSerMetGluArgAlaGlyLeuThrValPro 500

Qy   501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
         |||||||||||||||||||||||||||||||||||
Db  1567 AGGGCACATAGTCCGTTTGTGTTCCACTTGCAAGGATCGGCGTTGCATCTAAACTCCTT 1626

Qy   521 Ser 521
         |||
Db  1627 TCT 1629
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Db 1507 ATATTGAAAGGTGATGATGATGCCAAAGTTAGCATGGGAAGAGAGAGGACGTGGCCTCACAGTTCA 1566

RESULT 5
US-10-104-706-1
; Sequence 1, Application US/10104706
; GENERAL INFORMATION:
; APPLICANT: Odell, Joan
; APPLICANT: Yu, Xiaodan
; APPLICANT: Lu, Guihua
; APPLICANT: Xu, Hu
; APPLICANT: Ruff, Richard
; TITLE OF INVENTION: Root-Specific, Stimulant Inducible Promoter and its Use
; FILE REFERENCE: BB1468 US NA
; CURRENT APPLICATION NUMBER: US/10/104,706
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/278379
; PRIOR FILING DATE: March 23, 2001
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 1756
; TYPE: DNA
; ORGANISM: Glycine max
US-10-104-706-1

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Alignment Scores:
Pred. No.:
Score:                                1.51e-259     Length:        1756
Percent Similarity:                   2269.00       Matches:       454
Best Local Similarity:                87.14%        Conservative:  0
Query Match:                          87.14%        Mismatches:    67
DB:                                   94.70%        Indels:        0
                                      40            Gaps:          0

US-09-857-581-66 (1-521) x US-10-104-706-1 (1-1756)

Qy     1 MetLeuLeuGluGluLeuAlaLeuGlyLeu***ValLeuValAlaLeuPhe***HisLeuArgPro 20
         ||||||||||||||||||||||   |||||||||||   ||||||||||
Db    67 ATGTTGCTGGAACTTGCACTTGGTTTGTTGTGTTAGCCTTGTTTCTGCACTTGCGTGCC 126

Qy    21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
         ||||||   |||   ||||||||||||||||||||||||||||   |||
Db   127 ACACCAGTGCAAAATCAAAAGCACTTCGCCACTCCCAAACCCTCCAAGCCCAAAGCCT 186

Qy    41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysSerLeuLeuHisTyrAla*** 60
         ||||||||||||||||   ||||||||||||||||||||||||||||
Db   187 CGTCTTCCCTTCATTGGCCACCTTCACTTCTTAAAAGATAAACTTCTCCACTATGCACTC 246

Qy    61 IleAspLeuSerLysLysHisGlyProLeuPheSer******PheGlySerMetProThr 80
```

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                    |||||||||||||||||||||||||||||||||||||||||||||||||      |||||||||||||||||||
Db   247  ATCGAATCTCCAAAAAGCATGGCCCCTTATTCTCTCTTCGGCTCCATGCCAACC                                    306

Qy    81  ValValAlaSerThrProGlnLeuPheLeuGln******GluAlaThrSer                                        100
          |||||||||||||||||||||||||||||||||||      ||||||||||
Db   307  GTCGTTGCCTCCACCCTGAGTTGTTCAAGCTTCTTCCTCCAAACCACGAGGCAACTTCC                                366

Qy   101  Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp******ValAla                               120
          |||      ||||||||||||||||||      |||      |||||||||      ||||||
Db   367  TTCAACACAGGTTCCAAACCTTCGCCATTACACCGCTCACTTACCGACAACTCTGTGGCC                               426

Qy   121  ******Pro***GlyProTyrTrp***PheValArgGlyLeuIleMetAsnAspLeuLeu                               140
          ||||||   |||   |||||||||||   ||||||||||||||||||||||||||||||
Db   427  ATGGTTCCATTCCGACCTTACTGGAAGTTCGTTGAGGAAGCTCATCATGAACGACCTTCTC                              486

Qy   141  AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleuArgGly***Leu                              160
          ||||||||||||||||||   ||||||||||||||||||||||||||||||||||   |||
Db   487  AACCCCACCACCGTCAACAAGCTCAGGCCGTTTGAGGACCCCAACAGATCCCAAGTTCCTT                              546

Qy   161  Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeu                                  180
          |||      |||||||||      |||||||||   |||||||||||      ||||||||||
Db   547  AGGGTTATGGCCCAAAAGCGAGAGGCCCCAGAAGCCCTTGACGTCACCGAGGAGCTTCTC                               606

Qy   181  LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp                               200
          ||||||   |||||||||   |||||||||   ||||||||||||||||||||||||||||||
Db   607  AAATGGAACAACAGCACCATCTCCATGATGAATGCTCGGCGAGGCTGAGGAGAATCAGAGAC                             666

Qy   201  IleAlaArgGluValLeuLeuIle***GlyGluTyrSerLeuThrAspPheIle***Pro                               220
          ||||||||||||||||||||||   |||||||||||||||||||||||||   |||
Db   667  ATCGCTCGGCAGGTTCTTAAGATCTTCGGCGAATACAGCCTCACTGACTTCATCTGCCT                                726

Qy   221  LeuLys***LeuLysValGlyLysTyrArgIleuAspProAlaSerPheIleLeuAsnLysPhe                            240
          ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   727  TTGAAGTATCTCAAGGTTGGAAAGTATAGAGAGGAGGATTGAGAGATCTTGAACAAGTTC                               786

Qy   241  AspProValValGlu***ValIlelleLysLysArgAsp***IleValArgArgArg***Asn                            260
          |||||||||||||||   |||||||||||||||||||||||   ||||||||||||   |||
Db   787  GACCCTGTCGTTGAAAGGGTCATCAAGAAGAGGGATATCGTCAGAAGGAGGAAAAGAAC                                846

Qy   261  GlyGlu******GluGlyGlu***SerGlyVal***LeuAspThrLeuGluGluPheAla                               280
          |||||||||   |||||||||   |||||||||   ||||||||||||||||||||||||
Db   847  GGAGAAGGTTGTTGAGGGTGAGGGCCAGCCGCGGTTCTTCCTCGACACTTTGCTTGAATTCGCT                           906

Qy   281  GluAspGluThr***GlulleLysIleThrLys******IlelysGlyLeuValValAlaAsp                            300
          |||||||||||||   ||||||||||||||||||   |||||||||||||||||||||||
Db   907  GAGGACGAGACCATGGAAGATCAAAATTACCAAGGACGAAAATCAAGGGCCTTGTTGTCGAC                             966

Qy   301  ***PheSerAlaGly***AspSerThrAla******ThrGluTrpProAlaLeuAlaGluLeu                            320
          |||||||||||||   |||||||||||||||   |||||||||||||||||||||||||||
Db   967  TTTTTCTCGCAGGACAGATTCACACGCGTGGGCAACAGAGTGGCCATTGGCAGGCTC                                  1026

Qy   321  IleAlaAspGluThr***ValLeu******AlaArgGluGlu***TyrSerValValGlyLys                            340
          ||||||||||||||||   ||||||   |||||||||   |||||||||||||||||
Db  1027  ATCAACAATCCCAGGGTGTTCCAAAAGGCTCGTGAGGAGGTCTACAGTGTTGTGGGCAA                                1086

Qy   341  Asp***LeuValAspThrGlnAsnLeuProTyrIleuArgGlyAlaIleuValVallys                                360
          |||
Db                                                                                            1146
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```
Db  1087  GATAGACTCGTTGACGAAGTTGACACTCAAAACCTTCCTTACATTAGGGGCCATTGTGAAG                              1146

Qy   361  GluThrPheArgMetHisProProLeuProValValLysArgGlyLysCys***GluGluCys                            380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1147  GAGACATTCCGAATCGCACCCACCTCCACTTGGTTGTTCAAAAGAAGTTCACAGAGAGTGT                              1206

Qy   381  ***IleAsnGly***Val***ProGluGlyAlaLeu******PheAsnValTrpGlnVal                               400
          |||      |||      |||||||||      |||      |||||||||||||||||
Db  1207  GAGAATAATGGGTATCTGATCCCCAGAGGGAGCCATTGGTTCTTTCAATGTTTGGCAAGTA                              1266

Qy   401  Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu                               420
          |||      |||   ||||||||||||||||||||||   |||||||||||||||||||
Db  1267  GGAAGGGACCCCAAAATACTGGGACAGCAGACCATCAGAATTCCGTCCCGAGGAGGTTCTTAGAA                           1326

Qy   421  Thr***AlaGluGlyGluAla******LeuAspLeuArgGly***HisGlnLeuLeu                                  440
          |||      ||||||||||||||   ||||||||||||||   ||||||||||||
Db  1327  ACTGGTGCTGAAGGGGAAGGCAGCGGGCCTCTTGACCTTAGGGGGCAGCAATTCCAACTCCTC                             1386

Qy   441  ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala                               460
          |||||||||||||||||||   |||||||||||||||   ||||||||||||||||   |||
Db  1387  CCATTGGGTCTCTGGGACGAGGAATGTGCCCTGGGTGTCAATTGGCTACTTCAGGGAATGGCA                             1446

Qy   461  ThrLeuLeuAlaSerIleulleGlnCysPheAspLeuGlnValValLeuGlyProGlnGly***Gln                         480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1447  ACACTTCTTGCAATCTCTTATCCAATCGCTTTGACCTGGAAGGTGTGGGGCCCCTCAAGGACA                             1506

Qy   481  IleLeuLeuGly***AspAlaLysValSerMetGluGluuArgAlaGlyIleGlyThrValPro                            500
          |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db  1507  ATATTGAAAGGTGATGCATCCAAAGTTAGCATGGAAGAAGAGAGCTGGGCATCGGGAACTGTTCCA                          1566

Qy   501  ArgAlaHisSerLeuValCysValProLeuuAlaArglleGlyValAlaAlaSerLysLeuLeu                            520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1567  AGGGCACATAGTCTCGTTTGTGTTCCCACTTGCAAGGATCGGGGTTGCAGCTAGCAAACTCCTT                            1626

Qy   521  Ser                                                                                       521
          |||
Db  1627  TCT                                                                                       1629
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RESULT 6
US-10-104-706A-1

; Sequence 1, Application US/10104706A
; GENERAL INFORMATION:
; APPLICANT: Odell, Joan
; APPLICANT: Yu, Xiaodan
; APPLICANT: Lu, Guihua
; APPLICANT: Xu, Hu
; TITLE OF INVENTION: Root-Specific, Stimulant Inducible Promoter and its Use
; FILE REFERENCE: BB1468 US NA
; CURRENT APPLICATION NUMBER: US/10/104,706A
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/278379
; PRIOR FILING DATE: March 23, 2001
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Microsoft Office 97
SEQ ID NO 1
; LENGTH: 1756
; TYPE: DNA

; ORGANISM: Glycine max
US-10-104-706A-1

Alignment Scores:

Pred. No.:
Score: 1.51e-259
Score: 2269.00
Percent Similarity: 87.14%
Best Similarity: 87.14%
Best Local Similarity: 94.70%
Query Match: 40
DB:

Length: 1756
Matches: 454
Conservative: 0
Mismatches: 0
Indels: 67
Gaps: 0

US-09-857-581-66 (1-521) x US-10-104-706A-1 (1-1756)

```
Qy    1 MetLeuLeuGluLeuValAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro  20
        |||||||||||||||||||||||||||||||   |||||||||||||||   |||||||||||
Db   67 ATGTTGCTGGAACTTGCACTTGGTTTGTTTGTTGTTAGCTTGTTTCTGCACTTGGCTGCC    126

Qy   21 ThrPro***Ala***SerLysAlaleuArgHisLeuProAsnProSerPro***Pro       40
        |||   |||   |||||||||||||||||||||||||||||||||||   |||
Db  127 ACACCAAGTGCAAAATCAAAAGCACTTCGCCAACTTCCAAACCCTCCAAGCCCAAAGCCT    186

Qy   41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla***     60
        |||||||||||||||||||||   |||||||||||||||||||||||||
Db  187 CGTCTTCCCTTCATTGGCCACCTTCACCTCTTAAAAGATAAAACTTCTCCACTTATGACTC   246

Qy   61 IleAspLeuSerLysLysHisGlyProLeuPheSer******PheGlySerMetProThr     80
        |||||||||||||||||||||||||||||||||||      ||||||||||||||
Db  247 ATCGATCTCTCCAAAAAGCATGGGCCCCTTATTCTCTCTCTTCGGCTTCCATGCCAACC    306

Qy   81 ValValAlaLeuSerThrProGluLeuPheLysLeuPheLeuGln******GluAlaThrSer 100
        ||||||||||||||||||||||||||||||||||||||||      ||||||||||
Db  307 GTCGTTGCTCTCCACCCCGAGTTGTTCAAAGTTGTTCCCCAAACCCACCAGGCAACTTCC   366

Qy  101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp******ValAla   120
        |||   |||||||||||||||||||   |||   ||||||||||      ||||||
Db  367 TTCACAACAAGGTTCCAAACCTCTGCCATAAGACCCTCACTTACGACAACTCGTGGGC    426

Qy  121 ******Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeu   140
              |||   |||||||||||   ||||||||||||||||||||||||||||||
Db  427 ATGGTTCCAATTCGGACCTTACTGGAAGTTCGTGAGGAGCTCATCATGAACGACCTTCTC   486

Qy  141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu   160
        ||||||||||||||||||   |||||||||||||||||||||||||||||   |||
Db  487 AACGCCACCACCGTCAACAAGCTCAGGCCCTTGAGGACCCAACAGATCCGCAAGTTCCTT   546

Qy  161 Arg***MetAlaGln***AlaGluIla***LysProLeuAsp***ThrGluGluLeuLeu   180
        |||   ||||||||||   ||||||   ||||||||||   |||||||||||||||
Db  547 AGGGTTATGGCCCAAACGGAGAGGCCCCAGAAGCCCTTGACGTCACCGAGGAGTTCTC    606

Qy  181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp   200
        ||||||   |||||||||   |||||||||   |||||||||||||||||||||||||
Db  607 AAATGGACCAACAGCACCACCTCCATGATGATGCTCGGCGAGGCTGAGGAGATCAGAGAC   666

Qy  201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro   220
        ||||||||||||||||||||||   |||||||||||||||||||||||||   |||
Db  667 ATCGCTCGCGAGGTTCTTAAGATCTTCGGCGAAATACAGCCCTCACTGACTTCATCTGGCCT  726

Qy  221 LeuLys***LeuLysValAlaGlyLysTyrGluValGlySerGlyIleAspAspAspIleLeuAsnLysPhe  240
        ||||||   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  727 TTGAAGTANTCCAAGGTTGCAGGAAAGTATGAAGTTGGAAGTGGGATTGATGACGATATTCTGAACAAGTTC  786

Qy  241 AspProValValGluValAlaIleLysLysSerArg***IleValAlaArgArg***Asn   260
        ||||||||||||||||||||||||||||||||||   ||||||||||||||   |||
Db  787 GACCCTGTCGTTGAAGTGGCTATCAAGAAGTCCAGAGGCATCGTGGCAAGAAGAAAGAAC   846

Qy  261 GlyGlu******GluGlyGlu***SerGlyVal***LeuAspThrLeuGluPheAla     280
        ||||||      |||||||||   ||||||||||   |||||||||||||||||||
Db  847 GGAGAAGGTTGTTGAGGGCGAGGCCGAGGCGCGTCTTCCTCGACACTTTGCTTGAATTCGCT  906

Qy  281 GluAspGluThr***GluIleLysIleThrLys*****IleLysGlyLeuValLeuAsp   300
        |||||||||||   ||||||||||||||||||     |||||||||||||||||||
Db  907 GAGGACGAGACCATGGAGATCAAGATTACCAAGGACGAACAAATCAAGGGCCTTGTTCTCGAC  966

Qy  301 ***PheSerAlaGly***AspSerThrAla******ThrGluTrpProAlaLeuAlaGluLeu  320
           ||||||||||   ||||||||||      ||||||||||||||||||||||||||
Db  967 TTTTTCTCTGCAGGGACAGATCCCACGGGGCCAACAGAGTGGCCAGCGCTGGCAGAGCTC   1026

Qy  321 IleAsnAsnPro***ValLeu******AlaArgGluGlu***TyrSerValValGlyLys  340
        ||||||||||   ||||||      |||||||||||   ||||||||||||||
Db 1027 ATCAACAATCCCAGGGTGTTGGCAAAAGGCTTCGTGAGGAGGTCTACAGTGTTGTGGGCAAA 1086

Qy  341 Asp***LeuValAspGluValIleAspThrArgGlnAsnLeuProThrIleArgAlaIleLeuValLys 360
        |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1087 GATAGACTCGTTGACGAAGTTGACACTCAAAACCTTCCTACAATTAGGGCCATTCTGGTGAAG   1146

Qy  361 GluThrPheArgMetHisProProLeuProValValLysArgGlyCys***GluGluCys  380
        |||||||||||||||||||||||||||||||||||||||||||   |||||||
Db 1147 GAGACATTCCGAATCCACCCACCTCTCCCAGTCGTCAAAAGAAGTCCACAGAAGAGTGT    1206

Qy  381 ***IleAsnGly***Val***ProGluGlyAlaLeu******PheAsnValTrpGlnVal 400
           ||||||   |||   ||||||||||      |||||||||||||
Db 1207 GAGATTAATGGGTATGTGATCCCAGAGGGAGCATTGGTTCTCTTCAATGTTTGGCAAGTA   1266

Qy  401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluPheLeuGlu    420
        |||   |||   ||||||||||||||||||||   |||||||||||||||
Db 1267 GGAAGGGACCCCAAATACTGGGACAGACCATCAGAATTCCGTCCCGAGTTCTTAGAA    1326

Qy  421 Thr***AlaGluGlyGlyAla******LeuAspLeuArgGly***HisPheGlnLeuLeu 440
        |||   ||||||||||||||      ||||||||||||||   ||||||||||||||
Db 1327 ACTGGTGCTGAAGGGCAAGCAGGGCCCTCTTGANCTTAGGGGCCAGCATTCCAACTCCTC    1386

Qy  441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
        ||||||||||||||||   ||||||||||||   |||||||||||||   |||
Db 1387 CCATTTGGGTCTGGGAGAATGTGCCCGGTGTCAAATTGGCTACTTCAGGATAGGCA    1446

Qy  461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuValLeuGlyProGlnGlyGln     480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1447 ACACTTCTTGCATCTCTTATCCAATGCTTTGACCTGGTCCTGGGCCCTCAAGGACA    1506

Qy  481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
        |||||||||||   |||||||||||||||||||||||||||||||||||||||
Db 1507 ATATTGAAAGGTGATGCCAAGGTTAGCATGGAAGAGAGGGCTGGCCTCACAGTTCCA    1566

Qy  501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1567 ...
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Db  1567  AGGGCACATAGTCTCGTTGTTGTTGTTCCACTTGCAAGGAATGGGCGGCTTGCACTCTAAAACTCCTT  1626
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   521  Ser 521
          |||
Db  1627  TCT 1629
```

RESULT 7
US-10-171-174A-9

; Sequence 9, Application US/10171174A
; GENERAL INFORMATION:
; APPLICANT: Odell, Joan
; APPLICANT: Yu, Xiaodan
; TITLE OF INVENTION: A METHOD FOR ALTERING THE ISOFLAVONOID PROFILE IN THE
  PLANT PARTS
; TITLE OF INVENTION: OF AN ISOFLAVONOID-PRODUCING PLANT
; FILE REFERENCE: BB1452 US NA
; CURRENT APPLICATION NUMBER: US/10/171,174A
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 60/297,981
; PRIOR FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 1756
; TYPE: DNA
; ORGANISM: Glycine max
US-10-171-174A-9

Alignment Scores:
Pred. No.:
Score: 1.51e-259   Length: 1756
Percent Similarity: 2269.00   Matches: 454
Best Local Similarity: 87.14%   Conservative: 0
Query Match: 87.14%   Mismatches: 67
                       94.70%   Indels: 0
                       41   Gaps: 0
                                      DB:

US-09-857-581-66 (1-521) x US-10-171-174A-9 (1-1756)

Qy   1 MetLeuLeuGluLeuValAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
         |||||||||
Db   67 ATGTTGCTGGAACTTGGACTTGGTTGTTGTTAGCTTTGTTCTGCACTTGCGTCCC 126

Qy   21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
         |||||||||
Db 127 ACACCAAGTGCAAAATCAAAAGACACTTCGCCACTTCCCAAACCTTCCCAAGCCACAAGCCT 186

Qy   41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLlysLeuLeuHisTyrAla*** 60
         |||||||||
Db 187 CGTCTTCCCTCATTGGCCACACTTCACCTCTTAAAAGATAAACTTCCCACTATGGCACTC 246

Qy   61 IleAspLeuSerLysHisLeuGlyProLeuProPheSer******PheGlySerMetProThr 80
         |||||||||
Db 247 ATCGATCTCTCCAAAAAGCACAGGCCCCTTATTCTCTCTCGGGCTCCAATGGCCAACC 306

Qy   81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln******GluAlaThrSer 100
         |||||||||
Db 307 GTCGTTGCCTCCACCCCTGAGTTGTTCAAGCTCTTCCTCCAAACCACGAGGCAACTTCC 366

Qy 101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp******ValAla 120
         |||||||||
Db 367 TTCAACACAGGTTCCAAACCTTCGCCATAAGACGGCCCACTTACGACAACTCTGTGGCC 426

Qy 121 ******Pro***GlyProTyrTrp***PheValArgGlyLysLeuIleMetAsnAspLeuLeu 140
         |||||||||
Db 427 ATGGTTCCATTCGGACCTTACTCGGAAGTTCGTCGAGGAAGGTCATCATGAACGACCTTCTC 486

Qy 141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnIleIleArgLys***Leu 160
         |||||||||
Db 487 AACGCCACCACCGTCAACAAGCTCAGGCCCTTTGAGGAGGACCCCAACGATCCCAAGTTCCTT 546

Qy 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
         |||||||||
Db 547 AGGGTTATGGCCCAAAGCCACGAGGCGCCAGAAGCCCCTTGACGTCACCGAGGAGCTTCTC 606

Qy 181 LysTrp***AsnSerThr***SerMetMet***LeuGlyValAlaGlyGluIleArgAsp 200
         |||||||||
Db 607 AAATGGACCAACACAGCACCATCTCCAATGATGAATCTCGGCGGAGGCTGAGGAGGAGAGAC 666

Qy 201 IleAlaIleArgGluValIleLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
         |||||||||
Db 667 ATCGCCATCCGGAGGGTTCTTAAGATCTTCGGCGAATACAGCCCTCACTGACTTCATCTGGCCT 726

Qy 221 LeuLys***LeuLysValGlyLysTyrGluLysGlyArgIleAspAspIleLeuAsnLysPhe 240
         |||||||||
Db 727 TTGAAGTTATCTCAAGGTTGGAAAGTATGAGAAGGGTCGAATTGATGACATCCTTAACAAGTTC 786

Qy 241 AspProValValGlyLluArgValIleIleThr***IleValArgArgArg***Asn 260
         |||||||||
Db 787 GACCCTGTCGTTGGAAAGGTCATCAAGAAGAGGTCGAATGGTCAGAGGAGGAGAAGAAC 846

Qy 261 GlyGlu******GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
         |||||||||
Db 847 GGAGAAGTTGTTGAGGGCGAGGCCAGCAAGGGCGGGTCTTCCTCCACACTTTGCTTGAATTGGCT 906

Qy 281 GluAspGluThr***GlulleLysIleThrLys******IleLysGlyLeuValLysAsp 300
         |||||||||
Db 907 GAGGACGAGACAGGCATGGAGATCAAAATTACCAAGGGCAAATCAAAGGGCCTTGTTGTCGAC 966

Qy 301 ***PheSerAlaGly***AspSerThrAla******ThrGluTrpAlaLeuGluGlu 320
         |||||||||
Db 967 TTTTTCTCTGCAGGGACCAGATTCCACAGGGGTGGCAAACAGAGTGGCCATTGGAGGAGCTC 1026

Qy 321 IleAsnAsnPro***ValLeu******AlaArgGluGlu***TyrSerValValGlyLys 340
         |||||||||
Db 1027 ATCAACAATCCAGGGGTGTTGCAAAGGCGTCGGAGGAGGGTCTACAGTGTTGTCGGCAAA 1086

Qy 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProCytyrIleArgAlaIleValLys 360
         |||||||||
Db 1087 GATAGACTTCGTTGACGAAGTTGACACTCAAAACCTTCCTTACAATTAGGGCCATTGTGAAG 1146

Qy 361 GluThrPheArgMetHisProProLeuProValValLys***ArgGlyLysCys***GluGluCys 380
         |||||||||
Db 1147 GAGACATTCGAATTGCACCCACCACTCCCAGTTGGTCAAAAGAAAGTGCAAGAAGAGTGT 1206
```

Qy    381  ***IleAsnGly***Val***ProGluGlyAlaLeu******PheAsnValTrpGlnVal 400
           GAGATTAATGGGTATGTGATCCCAGAGGGAGCGGAGCATTGGTTCTTTCAATGTTGCAAGTA
Db   1207  GAGATTAATGGGTATGTGATCCCAGAGGGAGCGGAGCATTGGTTCTTTCAATGTTGCAAGTA 1266

Qy    401  Gly***Asp***LysTyrTrpAspArgProSerGlu****ArgProGluArgPheLeuGlu 420
           GGAAGGGACCCCAAATACTGGGACAGACCATCAGAATTCGGTCCCCGAGAGGTTCTTAGAA
Db   1267  GGAAGGGACCCCAAATACTGGGACAGACCATCAGAATTCGGTCCCCGAGAGGTTCTTAGAA 1326

Qy    421  Thr***AlaGluGlyGluAla******LeuAspLeuArgGly***HisPheGlnLeuLeu 440
           ACTGGTGCTGAGGGGGAAGCAGGGGCCCTTGATCTTAGGGGGCCAGCATTTCAAACTCCTC
Db   1327  ACTGGTGCTGAGGGGGAAGCAGGGGCCCTTGATCTTAGGGGGCCAGCATTTCAAACTCCTC 1386

Qy    441  ProPheGlySerGlyArg***AspAlaLysArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
           CCATTTGGGTCTGGGAGGGAGAATGTGCCCGTGTTCAATTTGGGTACTTCAGGAATGGCA
Db   1387  CCATTTGGGTCTGGGAGGGAGAATGTGCCCGTGTTCAATTTGGGTACTTCAGGAATGGCA 1446

Qy    461  ThrLeuIleuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
           ACACTTCTTGCCATCTCTTATCCAATGCTTTGACTGCAAGTGCCTGGGGGTCCAAGGACAA
Db   1447  ACACTTCTTGCCATCTCTTATCCAATGCTTTGACTGCAAGTGCCTGGGGGTCCAAGGACAA 1506

Qy    481  IleLeuLeuLysGly***AspAlaLysValSerMetCysGluValArgIleGlyValValAlaGlyValThrValPro 500
           ATATTGAAAGGTGATGATGCCAAAGTTAGCATGGAAGAGAGAGCTCTTCTCCAAACCACAG
Db   1507  ATATTGAAAGGTGATGATGCCAAAGTTAGCATGGAAGAGAGAGCTCTTCTCCAAACCACAG 1566

Qy    501  ArgAlaHisSerLeuVolCysValProLeuValArgIleLeuGlyValAlaGlyLeuThrLeuLeu 520
           AGGGCACACAGTCTCGTTGTTGTTCCACTTGCAAGGATACGGGGGTTGCATCTAAACTCCTT
Db   1567  AGGGCACACAGTCTCGTTGTTGTTCCACTTGCAAGGATACGGGGGTTGCATCTAAACTCCTT 1626

Qy    521  Ser 521
           TCT
Db   1627  TCT 1629

RESULT 8
US-60-117-769-1
; Sequence 1, Application US/60117769
; GENERAL INFORMATION:
; APPLICANT: Fader, Gary M.
; APPLICANT: McGonigle, Brian
; APPLICANT: Jung, Woosuk
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Isoflavone Synthase
; FILE REFERENCE: BB-1339-PI
; CURRENT APPLICATION NUMBER: US/60/117,769
; CURRENT FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Microsoft Word Version 7.0A
; SEQ ID NO 1
; LENGTH: 1756
; TYPE: DNA
; ORGANISM: Glycine max
US-60-117-769-1

Alignment Scores:
Pred. No.:               1.51e-259       Length:          1756
Score:                   2269.00         Matches:          454
Percent Similarity:      87.14%          Conservative:       0
Best Local Similarity:   87.14%          Mismatches:        67

Query Match:    94.70%      Indels:   0
DB:             55          Gaps:     0

US-09-857-581-66 (1-521) x US-60-117-769-1 (1-1756)

Qy      1  MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe****HisLeuArgPro 20
           ATGTTGCTGGAACTTGCACTGGGTTTGTTTGTTGCTAGCTTGTTCTGCACTTCCGTCCC
Db     67  ATGTTGCTGGAACTTGCACTGGGTTTGTTTGTTGCTAGCTTGTTCTGCACTTCCGTCCC 126

Qy     21  ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
           ACACCAAGTGCAAAATCAAAAAGCACTTCGCCACTCCAAAACCCTCCAAGTCCACCAAAGCCT
Db    127  ACACCAAGTGCAAAATCAAAAAGCACTTCGCCACTCCAAAACCCTCCAAGTCCACCAAAGCCT 186

Qy     41  ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla*** 60
           CGTCTTCCCTTCATTGGGCACCACTTCACCTCTTAAAAGATAAACTTCTCCACTATGCACTC
Db    187  CGTCTTCCCTTCATTGGGCACCACTTCACCTCTTAAAAGATAAACTTCTCCACTATGCACTC 246

Qy     61  IleAspLeuSerLysLysHisGlyProLeuPheSer******PheGlySerMetProThr 80
           ATCGATCTCTCCAAAAAGCATGGCCCCTTATTCTCTCTCCTTCGGCTCCATGCCAACC
Db    247  ATCGATCTCTCCAAAAAGCATGGCCCCTTATTCTCTCTCCTTCGGCTCCATGCCAACC 306

Qy     81  ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln******GluAlaThrSer 100
           GTCGTTGCCTCCACCCCTGAGTTGTTCAAGCTCTTCCTCCAAACCACCACGAGGGCAAACTTCC
Db    307  GTCGTTGCCTCCACCCCTGAGTTGTTCAAGCTCTTCCTCCAAACCACCACGAGGGCAAACTTCC 366

Qy    101  Phe****ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp******ValAla 120
           TTCAACACAAGGTTCCAAACCTCTGCCAGAACGCCTCACTTACGACACTCGTGGCC
Db    367  TTCAACACAAGGTTCCAAACCTCTGCCAGAACGCCTCACTTACGACACTCGTGGCC 426

Qy    121  ******Pro***GlyProTyrTrp****PheValArgLysLeuIleMetAsnAspLeuLeu 140
           ATGGTTCCATTCGGACCTTACTGGAAGTTCGTGAGGAAGTTCATCATGAACGACCTTCTC
Db    427  ATGGTTCCATTCGGACCTTACTGGAAGTTCGTGAGGAAGTTCATCATGAACGACCTTCTC 486

Qy    141  AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleLeuArgGlyLys***Leu 160
           AACCCCACCACCGTCAACAAGCTCAGGCCCTTGAGGACCCAACAGATCCCGCAAGTTCCTT
Db    487  AACCCCACCACCGTCAACAAGCTCAGGCCCTTGAGGACCCAACAGATCCCGCAAGTTCCTT 546

Qy    161  Arg***Met***AlaGln***AlaGluAla***LysProLeuAsp***ThrGluLeuLeu 180
           AGGGTTATGGGCCCAAAGGCCCAGAGCGCCCTTGACGTCACCGAGAGGCTTCTC
Db    547  AGGGTTATGGGCCCAAAGGCCCAGAGCGCCCTTGACGTCACCGAGAGGCTTCTC 606

Qy    181  LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluLeuArgAsp 200
           AAATGGACCAACAGACCACCATCTCCATGATGATGCTCGGCGAAGCTGAGGAGATCAGAGAC
Db    607  AAATGGACCAACAGACCACCATCTCCATGATGATGCTCGGCGAAGCTGAGGAGATCAGAGAC 666

Qy    201  IleAlaArgGluValIleLeuLysIle***GlyGluTyrSerLeuThrAspPhe***Pro 220
           ATCGCTCGCGAGGTTCTTAAGATCTTCGGCGAATACAGCCTCACTGACTTCATCTGGCCT
Db    667  ATCGCTCGCGAGGTTCTTAAGATCTTCGGCGAATACAGCCTCACTGACTTCATCTGGCCT 726

Qy    221  LeuLys***LeuLysValGlyLysTyrGlnLysArgIleuAspArgAspIleLeuAsnLysPhe 240
           TTGAAGTATCTCAAGGTTGGAAAGTATCAGAAGAGGATTGATAGAGACATTCTGAACAAGTTC
Db    727  TTGAAGTATCTCAAGGTTGGAAAGTATCAGAAGAGGATTGATAGAGACATTCTGAACAAGTTC 786

Qy    241  AspProValAlaGluArgValIleLeuLysLysArgArg***IleVolArgArgArg***Asn 260
           GACCCTGTTGCTGAAAGGGTCATCAAGAAGAGGCGCCGTGAGATCGTTCAGAAGAGAAAGAAC
Db    787  GACCCTGTTGCTGAAAGGGTCATCAAGAAGAGGCGCCGTGAGATCGTTCAGAAGAGAAAGAAC 846

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Qy     261  GlyGlu******GluGlyGlu***SerGlyVal****LeuAspThrLeuLeuGluPheAla  280
                |||||||                ||||||||                    ||||||||||||||
Db     847  GGAGAAGTTGCTTGAGGGCGAGGGCCAGCGCGGCGTCTTCCCGACACTTTGCTTGAATTCGCT  906

Qy     281  GluAspGluThr***GluIleLysIleThrLys*******IleLysGlyLeuValValAsp  300
                ||||||||||||                |||||||                    |||||||||||||
Db     907  GAGGACGAGGACCATGGAGATCAAAATTACCAAGGAGACAAATCAAGGGCCTTGTTGTCGAC  966

Qy     301  ***PheSerAlaGly******AspSerThrAla******ThrGluTrpAlaLeuAlaGluLeu  320
                   |||||||||                |||||||              ||||||||||||||
Db     967  TTTTTCTCTGCAGGGACAGAGTTCCAGGGCCAAACAGAGTGGGCATTGGCAGAGCTC  1026

Qy     321  IleAsnAsnPro***ValLeu******AlaArgGluGlu***TyrSerValValGlyLys  340
                |||||||||||||                |||||||              ||||||||||||||
Db    1027  ATCAACAATCCCAGGGTGTTGCAAAAGGCTCGTGAGGAGTCTACAGTGTTGTGGGCAAA  1086

Qy     341  Asp***LeuValAspGluValAlaAspThrGlnAsnLeuProTyrIleArgAlaIleValLys  360
                      ||||||||||||||                |||||||              |||||||
Db    1087  GATAGACTCGTTGACGAGTTGACACTCAAAAACTTCCTTACATTAGGCCCATTGTGAAG  1146

Qy     361  GluThrPheArgMetHisProProLeuProValValLysArgGlyCys***GluGluCys  380
                |||||||||||||||                |||||||              |||||||
Db    1147  GAGACATTCCGAATGCACCCACCACTCCCAGTGGTCAAAAAGAAGGTGCACGAAGAGTGT  1206

Qy     381  ***IleAsnGly***Val***ProGluGlyValAlaLeu******PheAsnValTrpGlnVal  400
                   |||||||                |||||||              |||||||
Db    1207  GAGATTAATGGGTATGGTAGTCCAGAGGGGGTAGCCATTGGTTCTTTCAATGTTTGGCAAGTA  1266

Qy     401  Gly***Asp***LysTyrTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu  420
                   |||                |||||||              |||||||
Db    1267  GGAAGGGACCCCAAATACTGGGACAGACACATCAGAATTCCGTCCCGAGAGGTTCTTAGAA  1326

Qy     421  Thr***AlaGluGlyGluAla******Gly***LeuAspLeuArgGly***HisPheGlnLeuLeu  440
                      |||||||                |||||||              |||||||
Db    1327  ACTGCTGCTGAAGGGGAAGCAGGGCCTCTTGATCTTAGGGGCCCAGCATTTCAAACTCCTC  1386

Qy     441  ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala  460
                |||||||||||||||                |||||||              |||||||
Db    1387  CCATTTGGGTCTCGGGACGGAGGAAATGCCCCGGGTGTTCAATTTGGCTACTTCAGGAATGGCA  1446

Qy     461  ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln  480
                |||||||||||||||                |||||||              |||||||
Db    1447  ACACTTCTTGCATCTCTTATCCAANTGCTTTGACCTGCAAGTCCTGGGGCCCTCAAGGACAA  1506

Qy     481  IleLeuLeuLysGly***AspAlaLysSerValSerMetGluGlnArgAlaGlyLeuThrValPro  500
                |||||||||||||  .                |||||||              |||||||
Db    1507  ATATTGAAAGGTGATGAGGTCAAGTTAAGCATGGAACAGAGAGCTGGCCTACAGTTCCA  1566

Qy     501  ArgAlaHisSerLeuValCysValProLeuLeuArgIleGlyValAlaSerLysSerLeuLeu  520
                |||||||||||||||                |||||||              |||||||
Db    1567  AGGGCACATAGTCTCGTTTGTTTGTTCCACTTGCAAGGATCGGCGTTGCAATCATAAACTCCTT  1626

RESULT 9

Qy     521  Ser  521
                |||
Db    1627  TCT  1629
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